

REMARKS

Favorable reconsideration, reexamination, and allowance of the present patent application are respectfully requested in view of the foregoing amendments and the following remarks. The foregoing amendments do not add new matter and are fully supported by the originally filed claims, page 8, lines 20-24, page 15, lines 8-20, page 16, lines 13-23, page 17, lines 1-6, page 18, lines 10-15.

Objection to the Specification

At page 2 of the Office Action, the disclosure as a whole was objected to because it allegedly contains an embedded hyperlink and/or other form of browser-executable code. Applicant respectfully requests reconsideration of this objection.

The specification has been amended to remove portions of the embedded hyperlink in each instance, so that it is no longer browser-executable.

For at least the foregoing reasons, Applicant respectfully submits that the disclosure as a whole is not objectionable, and therefore respectfully requests withdrawal of the objection thereto.

Rejection under 35 U.S.C. § 112, second paragraph

In the Office Action, beginning at page 2, Claims 1-10 were rejected under 35 U.S.C. § 112, second paragraph, as reciting subject matters that allegedly are indefinite, more specifically in the recitation of “an ArcA protein does not normally function”, and “wherein the ArcA protein that normally functions is a protein”. Applicant respectfully requests reconsideration of this rejection.

The claims have been amended to recite “the production of ArcA protein is reduced or eliminated” and have further clarified the antecedent phrases. This amendment is based on the description at page 15, lines 16-18 of the specification. Applicants assert that the claims are definite and clear in its meaning and intent.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-10 fully comply with 35 U.S.C. § 112, second paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

In the Office Action, beginning at page 3, Claim 6 was further rejected under 35

U.S.C. § 112, second paragraph, as reciting subject matters that allegedly are indefinite. Applicant respectfully requests reconsideration of this rejection. Claim 6 was further rejected as being allegedly vague and indefinite in the recitation of “DNA hybridizable with the nucleotide sequence of nucleotide numbers 101 to 817 of SEQ ID NO: 31...”. Claim 6 has been amended by deletion of the allegedly indefinite phrases and insertion of the specific stringent conditions, and therefore, applicants assert this claim is definite and clear in its intent and meaning.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-10 fully comply with 35 U.S.C. § 112, second paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

Rejection under 35 U.S.C. § 112, first paragraph

In the Office Action, beginning at page 4, Claims 1-6 and 8-10 were rejected under 35 U.S.C. § 112, first paragraph, as reciting subject matters that allegedly fail to comply with the written description requirement. Applicant respectfully requests reconsideration of this rejection.

Attached as Exhibit A are alignments of ArcA protein *E. coli* with that of the other γ -proteobacteria. This data clearly demonstrates that the amino acid sequence of ArcA protein is highly conserved among γ -proteobacteria. As such, a person skilled in the art can obtain the homologous arcA gene from γ -proteobacterium other than *E. coli* and *Pantoea ananatis* based on the disclosed nucleotide sequence of arcA gene of *E. coli* (SEQ ID NO: 31) or *Pantoea ananatis* (SEQ ID NO:19), and use the obtained arcA gene to disrupt a chromosomal arcA gene in each γ -proteobacterium. Applicants assert the the description of SEQ ID NO:31 and SEQ ID NO:19 are sufficient to describe the genus of ArcA genes/proteins from other γ -proteobacterium, as one of skill in the art would be able to ascertain other species and their respective ArcA gene/protein sequences. Therefore, these two exemplified and described sequences constitute a representative number of species since the relevant structural properties are easily ascertained and determined due to the highly homologous nature of the ArcA genes/proteins among γ -proteobacterium.

Similarly, applicants assert that the description of *E. coli* and *Pantoea ananatis*

which have been modified so that an ArcA protein does not function normally are sufficient to adequately describe the genus of γ -proteobacterium encompassed by the claims. Specifically, as shown in the attached Exhibit A, the common feature of this genus of bacteria is their structural commonality of having a disrupted ArcA gene/protein. This common structural feature is present in any species of the genus, and is therefore sufficient to demonstrate possession of the genus of γ -proteobacterium.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-6 and 8-10 fully comply with 35 U.S.C. § 112, first paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

Rejection under 35 U.S.C. § 102(b)

In the Office Action, beginning at page 6, Claims 1-9 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Cotter et al. Applicant respectfully requests reconsideration of this rejection.

Claim 1 relates to a γ -proteobacterium including, *inter alia*, “a target substance synthesized via TCA cycle” and “as compared to a wild-type γ -proteobacterium”. Support for the subject matter in claim 1 can be found, e.g., at page 8, lines 23-24, and page 17, lines 4-6. Although Cotter et al. discloses arcA gene-disrupted strains, the strains described by Cotter et al. do not have an ability to produce a target substance synthesized via the tricarboxylic acid cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via the tricarboxylic acid cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant strain as described in page 9, lines 23-24 of the specification, and the MG1655 Δ sucA strain in which sucA gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-9 are not anticipated by Cotter et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 7, Claims 1-10 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Iuchi et al. Applicant respectfully requests reconsideration of this rejection.

As stated above, the claims recite “a target substance synthesized via TCA cycle” and “as compared to a wild-type γ -proteobacterium”. Although Iuchi et al. discloses *arcA* gene-disrupted strains, the strains disclosed by Iuchi et al. do not have an ability to produce a target substance synthesized via TCA cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via TCA cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant strain as described in page 9, lines 23-24 of the English specification, and the MG1655 Δ *sucA* strain in which *sucA* gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the English specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-10 are not anticipated by Iuchi et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 6, Claims 1-10 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Nystrom et al. Applicant respectfully requests reconsideration of this rejection.

Similar to our arguments presented above, the claims recite “a target substance synthesized via TCA cycle” and “as compared to a wild-type γ -proteobacterium”. Although Nystrom et al. discloses *arcA* gene-disrupted strains, Nystrom et al. does not disclose strains which have an ability to produce a target substance synthesized via TCA cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via TCA cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant

strain as described in page 9, lines 23-24 of the English specification, and the MG1655Δ sucA strain in which sucA gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the English specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-10 are not anticipated by Nystrom et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 8, Claim 2 was rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Sugimoto et al.. Applicants note that the patent number listed on page 8 of the office action is incorrect. The correct patent number, which is listed correctly on the PTO-892, is 5,919,694. Applicant respectfully requests reconsideration of this rejection.

Claim 2 has been amended to limit the number of amino acid substitutions, deletions or insertions to “up to 10”. Therefore, this limitation clearly removes the disclosure of Sugimoto et al. as prior art.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claim 2 is not anticipated by Sugimoto et al., is therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

Rejection under 35 U.S.C. § 102(e)

In the Office Action, beginning at page 9, Claims 1-10 were rejected under 35 U.S.C. § 102(e), as reciting subject matters that allegedly are anticipated by Cervin et al. Applicant respectfully requests reconsideration of this rejection.

Applicants hereby submit a translation of the priority documents and a verification by the translator, as Exhibit B. These documents are sufficient to effectively remove Cervin et al. as prior art since the priority date of July 12, 2002 can be relied upon by applicants, because the priority documents provide support for the claimed subject matter.

For at least the foregoing reasons, Applicant respectfully submits that the subject

matters of Claims 1-10 are not anticipated by Cervin et al., because Cervin et al. is not prior art to the claimed subject matter and therefore the claims are not unpatentable under 35 U.S.C. § 102(e), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(e).

Conclusion

For at least the foregoing reasons, Applicant respectfully submits that the present patent application is in condition for allowance. An early indication of the allowability of the present patent application is therefore respectfully solicited.

If Examiner Vogel believes that a telephone conference with the undersigned would expedite passage of the present patent application to issue, she is invited to call on the number below.

It is not believed that extensions of time are required, beyond those that may otherwise be provided for in accompanying documents. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and the undersigned respectfully authorizes that our deposit account 50-3077 be charged any required fees.

Respectfully submitted,

By: 
Shelly Guest Cermak

Shelly Guest Cermak
Registration No. 39,571

U.S. P.T.O. Customer No. 38108
Cermak & Kenealy, LLP
515 E. Braddock Road, Suite B
Alexandria, VA 22314
703.778.6608

Date: June 10, 2005

EXHIBIT A

ALIGNMENT DATA

In the alignment data, each accession number means the following species of γ -proteobacterium.

S4704	Shigella flexneri_2457T
SF4433	Shigella flexneri
C5488	E. coli_CFT073
ECs5359	E. coli_O157J
Z6004	E. coli_O157
JW4364	E. coli_J
B4401	E. coli
STM4598	Salmonella typhimurium
SC4443	Salmonella enterica subsp. enterica serovar Choleraesuis
T4637	Salmonella enterica subsp. enterica serovar Typhi Ty2
STY4947	Salmonella enterica subsp. enterica serovar Typhi
SPA4408	Salmonella enterica subsp. enterica serovar Paratyphi
YPTB0601	Yersinia pseudotuberculosis
YP3725	Yersinia pestis biovar Medievalis
Y3721	Yersinia pestis KIM
YP00458	Yersinia pestis
ECA3893	Erwinia carotovora
Plu0562	Photorhabdus luminescens
VC2368	Vibrio cholerae
VP0489	Vibrio parahaemolyticus
PBPRA0547	Photobacterium profundum
VF2120	Vibrio fischeri
VV0646	Vibrio vulnificus YJ016
VV10548	Vibrio vulnificus
PM0219	Pasteurella multocida
SO3988	Shewanella oneidensis
MS1504	Mannheimia succiniciproducens
HD0278	Haemophilus ducreyi
HI0884	Haemophilus influenzae
VF1570	Vibrio fischeri

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC; negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) (A)
(238 letters)

Database: GENES+DGENES: GENES+DGENES (amino acid sequence)
1,405,264 sequences; 537,705,622 total letters

Searching.....done

Sequences producing significant alignments:

Top 10	<input type="checkbox"/> Clear	Select operation	<input type="checkbox"/> Exec	Score	E
				(bits)	Value
<input checked="" type="checkbox"/> <u>sfx:S4704</u> arcA; negative response regulator of genes in aerobic ...				478	e-134
<input checked="" type="checkbox"/> <u>sfl:SF4433</u> arcA; negative response regulator of genes in aerobic...				478	e-134
<input checked="" type="checkbox"/> <u>ecc:c5488</u> arcA; aerobic respiration control protein arcA [KO:K02...				478	e-134
<input checked="" type="checkbox"/> <u>ecs:ECs5359</u> negative response regulator of genes in aerobic path...				478	e-134
<input checked="" type="checkbox"/> <u>ece:Z6004</u> arcA; negative response regulator of genes in aerobic ...				478	e-134
<input checked="" type="checkbox"/> <u>ecj:JW4364</u> arcA; Aerobic respiration control protein ArcA (Dye r...				478	e-134
<input checked="" type="checkbox"/> <u>eco:b4401</u> arcA, dye, fexA, msp, seg, sfrA, cpxC; negative respon...				478	e-134
<input checked="" type="checkbox"/> <u>stm:STM4598</u> arcA; response regulator (OmpR family) in two-compon...				477	e-134
<input checked="" type="checkbox"/> <u>sec:SC4443</u> arcA; response regulator (OmpR family) in two-compone...				477	e-134
<input checked="" type="checkbox"/> <u>stt:t4637</u> arcA; global response regulator [KO:K02483]				477	e-134
<input type="checkbox"/> <u>sty:STY4947</u> arcA; global response regulator [KO:K02483]				477	e-134
<input type="checkbox"/> <u>spt:SPA4408</u> arcA; global response regulator [KO:K02483]				474	e-133
<input type="checkbox"/> <u>yps:YPTB0601</u> arcA; response regulator (OmpR family), in two-comp...				445	e-124
<input type="checkbox"/> <u>ypm:YP3725</u> arcA; aerobic respiration control protein [KO:K02483]				445	e-124
<input type="checkbox"/> <u>ypk:y3721</u> arcA; negative response regulator of genes in aerobic ...				445	e-124
<input type="checkbox"/> <u>ype:YPO0458</u> arcA, dye, fexA, sfrA, seg, msp, cpxC; aerobic respi...				445	e-124
<input type="checkbox"/> <u>eca:ECA3893</u> arcA, cpxC, dye, fexA, msp, sfrA; aerobic respiratio...				445	e-124
<input type="checkbox"/> <u>plu:plu0562</u> arcA; negative response regulator of genes in aerobic...				442	e-123
<input type="checkbox"/> <u>vch:VC2368</u> fexA; aerobic respiration control protein FexA [KO:KO...				427	e-119
<input type="checkbox"/> <u>vpa:VP0489</u> fexA; aerobic respiration control protein FexA [KO:KO...				417	e-116
<input type="checkbox"/> <u>ppr:PBPR0547</u> fexA; putative aerobic respiration control protein...				412	e-114
<input type="checkbox"/> <u>vfi:VF2120</u> arcA; aerobic respiration control protein ArcA [KO:KO...				411	e-114
<input type="checkbox"/> <u>vvy:VV0646</u> fexA; aerobic respiration control protein FexA [KO:KO...				411	e-114
<input type="checkbox"/> <u>vvu:VV10548</u> fexA; aerobic respiration control protein FexA [KO:K...				411	e-114
<input type="checkbox"/> <u>pmu:PM0219</u> arcA; aerobic respiration control protein [KO:K02483]				394	e-108
<input type="checkbox"/> <u>son:S03988</u> arcA; aerobic respiration control protein ArcA [KO:KO...				392	e-108
<input type="checkbox"/> <u>msu:MS1504</u> ompR; response regulators consisting of a CheY-like r...				382	e-105
<input type="checkbox"/> <u>hdu:HD0278</u> arcA; aerobic respiration control protein ArcA [KO:K0...				377	e-103
<input type="checkbox"/> <u>hin:HI0884</u> arcA; aerobic respiration control protein arcA homolo...				374	e-103
<input type="checkbox"/> <u>vfi:VF1570</u> torR; TorCAD operon transcriptional regulatory protei...				217	2e-55

>sfx:S4704 arcA; negative response regulator of genes in aerobic pathways
(sensors, ArcB and CpxA) [KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPE||ATIHGEGRFCGDLED 238
SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPE||ATIHGEGRFCGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPE||ATIHGEGRFCGDLED 238

>sfl:SF4433 arcA; negative response regulator of genes in aerobic pathways
(sensors, ArcB and CpxA) [KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGK1Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPE||ATIHGEGRFCGDLED 238
SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPE||ATIHGEGRFCGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDTIRRIRKHFESTPDTPE||ATIHGEGRFCGDLED 238

>ecc:c5488 arcA; aerobic respiration control protein arcA [KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238

>ecs:Ec5359 negative response regulator of genes in aerobic pathways ArcA
[KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238

>ece:Z6004 arcA; negative response regulator of genes in aerobic pathways,
(sensors, ArcB and CpxA) [KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238

>ecj:JW4364 arcA; Aerobic respiration control protein ArcA (Dye resistance
protein) [KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238

>eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC; negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA)
[KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL|GPDGEQYKLPSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238
SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPE||ATIHGEGYRFCGDLED 238

>stm:STM4598 arcA; response regulator (OmpR family) in two-component regulatory system with ArcB (or CpxA), regulates genes in aerobic pathways [KO:K02483]
Length = 238

Score = 477 bits (1227), Expect = e-134
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180
TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL|D 238
SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL+D
Sbjct: 181 SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL|D 238

>sec:SC4443 arcA; response regulator (OmpR family) in two-component regulatory system with ArcB (or CpxA), regulates genes in aerobic pathways
Length = 238

Score = 477 bits (1227), Expect = e-134
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180
TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL|D 238
SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL+D
Sbjct: 181 SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL|D 238

>stt:t4637 arcA; global response regulator [KO:K02483]
Length = 238

Score = 477 bits (1227), Expect = e-134
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180
TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q
Sbjct: 121 TMNLGTVSEERRSVESYKFNGWELD|NSRSL|GPDGEQYKLPSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL|D 238
SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL+D
Sbjct: 181 SRAELKKMTGRELKPHRTVDVT|RR|RKHFESTPDTPE||AT|HGEGYRFCGDL|D 238

>sty:STY4947 arcA; global response regulator [KO:K02483]
Length = 238

Score = 477 bits (1227), Expect = e-134

Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENPGK|Q 180
TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENPGK|Q
Sbjct: 121 TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDVT|RR|RKHFESTPDTPE|I|AT|HGEGYRFGDLED 238
SRAELKKMTGRELKPHDRTVDVT|RR|RKHFESTPDTPE|I|AT|HGEGYRFGDLD+D
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVT|RR|RKHFESTPDTPE|I|AT|HGEGYRFGDLDQD 238

>spt:SPA4408 arcA; global response regulator [KO:K02483]

Length = 238

Score = 474 bits (1219), Expect = e-133
Identities = 236/238 (99%), Positives = 237/238 (99%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK 60
MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK
Sbjct: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENPGK|Q 180
TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENPGK|Q
Sbjct: 121 TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENSGK|Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDVT|RR|RKHFESTPDTPE|I|AT|HGEGYRFGDLED 238
SRAELKKMTGRELKPHDRTVDVT|RR|RKHFESTPDTPE|I|AT|HGEGYRFGDLD+D
Sbjct: 181 SRAELKKMTGRELKPHDRTVDVT|RR|RKHFESTPDTPE|I|AT|HGEGYRFGDLDQD 238

>yps:YPTB0601 arcA; response regulator (OmpR family), in two-component regulatory system with ArcB (or CpxA), regulates genes in aerobic respiration [KO:K02483]

Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKS|FEAEGYDVFEATDGAEMHQ|LSEYD|NLV|MD|NLPK 60
MQTPHILIVEDE+VTRNTLKS|FEAEGY V+EA DGAEMH ILSE DINLV|MD|NLPK
Sbjct: 1 MQTPHILIVEDE+VTRNTLKS|FEAEGY VVYEANDGAEMHH|LSEND|NLV|MD|NLPK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDK|LGLE|GADDY|TKPFNPRELT|RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFGWELD|NSRSL|GPDGEQYKLP|PRSEFRAMLHFCENPGK|Q 180
TMNL +V EERR VESYKFGWELD|NSRSL+ P GE YKLP|PRSEFRAMLHFCENPGK|Q
Sbjct: 121 TMNLSSVGEERRLVESYKFGWELD|NSRSL|SPTGEHYKLP|PRSEFRAMLHFCENPGK|Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLE+
Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLEE 238

>ypm:YP3725 arcA; aerobic respiration control protein [KO:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKS1FEAEGY V+EA DGAEMH ILSE DINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDEVTRNTLKS1FEAEGYVYYANDGAEMHHILSENDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
TMNL +V EERR VESYKFNGWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGK1Q
Sbjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVSPTGEHYKLPSEFRAMLHFCENPGK1Q 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLE+
Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLEE 238

>ypk:y3721 arcA; negative response regulator of genes in aerobic pathways, sensors, ArcB and CpxA [KO:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKS1FEAEGY V+EA DGAEMH ILSE DINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDEVTRNTLKS1FEAEGYVYYANDGAEMHHILSENDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLE|GADDY|TKPFNPRELT|RARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
TMNL +V EERR VESYKFNGWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGK1Q
Sbjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVSPTGEHYKLPSEFRAMLHFCENPGK1Q 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLE+
Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIRKFESTPDTPEIIATIHGEGYRFCGDLEE 238

>ype:YP00458 arcA, dye, fexA, sfrA, seg, msp, cpxC; aerobic respiration control protein [KO:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKS1FEAEGY V+EA DGAEMH ILSE DINLVIMDINLPGK

Subjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAEQYVVYEANDGAEMHHILSENDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Subjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNL +V EERR VESYKFNGWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGKIQ
Subjct: 121 TMNLSSVGEERRLVESYKFNGWELDINSRSLVSPTEHYKLPSEFRAMLHFCENPGKIQ 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLE+
Subjct: 181 SRGELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLEE 238

>eCA:ECA3893 arcA, cpxC, dye, fexA, msp, sfrA; aerobic respiration control protein [KO:K02483]
Length = 238

Score = 445 bits (1144), Expect = e-124
Identities = 224/238 (94%), Positives = 228/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAEQYV EATDGAEMH ILSE DINLVIMDINLPGK
Subjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYVVHEATDGAEMHHILSENDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQA VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Subjct: 61 NGLLLARELREQATVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNLG+ +EERR VESY+FNGWELDINSRSLI P GEQYKLPSEFRAMLHFCENPGKIQ
Subjct: 121 TMNLGSGTEERRLVESYRFNGWELDINSRSLISPAGEQYKLPSEFRAMLHFCENPGKIQ 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLED 238
SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLE+
Subjct: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTADTPEIATIHGEGYRFCGDLEN 238

>plu:plu0562 arcA; negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) (dye resistance protein) [KO:K02483]
Length = 238

Score = 442 bits (1138), Expect = e-123
Identities = 221/237 (93%), Positives = 226/237 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKSIFEAEQYV+EATD+G+EMH ILS DINLVIMDINLPGK
Subjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAEQYIVYEATDGESEMHILSNNDINLVIMDINLPGK 60
Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Subjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
TMNL VSEERR VESYKFNGWELDINSRSLI P GE YKLPRSEFRAMLHFCENPGKIQ
Subjct: 121 TMNLNSVSEERRQVESYKFNGWELDINSRSLISPAGEPYKLPSEFRAMLHFCENPGKIQ 180
Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLE 237
+RA+LLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIATIHGEGYRFCGDLE
Subjct: 181 TRADLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTMEIATIHGEGYRFCGDLE 237

>vch:VC2368 fexA; aerobic respiration control protein FexA [KO:K02483]
Length = 238

Score = 427 bits (1098), Expect = e-119
Identities = 210/238 (88%), Positives = 223/238 (93%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1ILSEYD1NLV1MD1NLPKG 60
MQTP ILIVEDE VTRNTLKS1FEAEGY VFEA++G EMHQ+LS+ INLV1MD1NLPKG
Sbjct: 1 MQTPQILIVEEQVTRNTLKS1FEAEGYAVFEASNGEEMHQVLSDYP1NLV1MD1NLPKG 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
+M+ GT EE+RSVE Y FNGWELD1NSRSL+ PDG+ YKLPRSEFRA+LHFCEPGK1Q
Sbjct: 121 SMHAGTTQEEKRSVEKYVFNGWELD1NSRSLVSPDGDSYKLPSEFRALLHFCENPGK1Q 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPEI1AT1HGEGYRFGDLED 238
+RA+LLKKMTGRELKPHDRTVDVT1RR1RKHFES TPEI1AT1HGEGYRFGDLED
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVT1RR1RKHFESVSGTPEI1AT1HGEGYRFGDLED 238

>vpa:VP0489 fexA; aerobic respiration control protein FexA [KO:K02483]
Length = 238

Score = 417 bits (1073), Expect = e-116
Identities = 206/238 (86%), Positives = 219/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1ILSEYD1NLV1MD1NLPKG 60
MQTP ILIVEDE VTRNTLKS1FEAEGY VFEA+DG EMHQ+LS+ INLV1MD1NLPKG
Sbjct: 1 MQTPQILIVEEQVTRNTLKS1FEAEGYAVFEASDGEEMHQVLSDNS1NLV1MD1NLPKG 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120
NGLLLARELREQAN+VALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR
Sbjct: 61 NGLLLARELREQAN1ALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
+M+ V EE+RSVE Y+FNGW LD1NSRSL+ P G+ YKLPRSEFRA+LHFCEPGK1Q
Sbjct: 121 SMSTNAVQEEKRSVEKYEFNGWVLD1NSRSLVSPAGDSYKLPSEFRALLHFCENPGK1Q 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPEI1AT1HGEGYRFGDLED 238
+RA+LLKKMTG ELKPHDRTVDVT1RR1RKHFES TPEI1AT1HGEGYRFGDLED
Sbjct: 181 TRADLLKKMTGGELKPHDRTVDVT1RR1RKHFESVSGTPEI1AT1HGEGYRFGDLED 238

>ppr:PPRA0547 fexA; putative aerobic respiration control protein FexA [KO:K02483]
Length = 239

Score = 412 bits (1060), Expect = e-114
Identities = 199/238 (83%), Positives = 220/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1ILSEYD1NLV1MD1NLPKG 60
MQTPHILIVEDE VTRNTLKS1FEAEGY VFEA DGAEMHQ+LSE+ ++LV1MD1NLPKG
Sbjct: 1 MQTPHILIVEDEHVTNTLKS1FEAEGYTVFEANDGAEMHQMLSEHPVHLV1MD1NLPKG 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLSR 120
NGLLLARELREQ ++ALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLL+R
Sbjct: 61 NGLLLARELREQGDMALMFLTGRDNEVDK1LGLE1GADDY1TKPFPRELT1RARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
MN G +E+++ VE Y+FNGW L+INSRSL+ P G+Q+KLPSEFRA+LHFCENPGKIQ
Sbjct: 121 AMNQGLPTEDKKLVERYFNGWSLEINSRSLVSPSGDQFKLPSEFRALLHFCENPGKIQ 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLED 238
+R +LLKKMTGRELKPHDRTVDVTIRRIRKHFES DTPEI+ATIHGEGYRFCGDLE +
Sbjct: 181 TRGDLLKKMTGRELKPHDRTVDVTIRRIRKHFESVADTPEIVATIHGEGYRFCGDLE 238

>yfi:VF2120 arcA; aerobic respiration control protein ArcA [KO:K02483]
Length = 239

Score = 411 bits (1056), Expect = e-114
Identities = 200/238 (84%), Positives = 220/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTP ILIVEDE VTRNTLKSIFEAEQY+VFEA+DG EMH++LSE +NLVIMDINLPGK
Sbjct: 1 MQTPQILIVEDEHVTTRNTLKSIFEAEQYNVFEASDGEEMHKVLSEQQLNLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELRE+ ++ALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLL+R
Sbjct: 61 NGLLLARELREQGDALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
+MN TV E+++ VE Y FNGW ++INSRSL+ P GE YKLPSEFRA+LHFCENPGKIQ
Sbjct: 121 SMNQNTVVEDKKMVERYVFNGWTVEINSRSLVSPSGESYKLPSEFRALLHFCENPGKIQ 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLED 238
+RA+LLKKMTGRELKPHDRTVDVTIRRIRKHFES DTPEI+ATIHGEGYRFCGDLE+
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRIRKHFESVDTPEIATIHGEGYRFCGDLEE 238

>yvy:VV0646 fexA; aerobic respiration control protein FexA [KO:K02483]
Length = 238

Score = 411 bits (1056), Expect = e-114
Identities = 205/237 (86%), Positives = 218/237 (91%)

Query: 1 MOTPHILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MOTP ILIVEDE VTRNTLKSIFEAEQY VFEA++G EMH +LSE +NLVIMDINLPGK
Sbjct: 1 MOTPQILIVEDEQVTRNTLKSIFEAEQYAVFEASNGDEMHHMLSENSINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPSEFRAMLHFCENPGKIQ 180
+M+ + EE+RSVE Y+FNGW LDINSRSLI P G+ YKLPSEFRA+LHFCENPGKIQ
Sbjct: 121 SMSSSVMPEEKRSVEKYEFGWLDINSRSLISPSSGDGYKLPSEFRALLHFCENPGKIQ 180

Query: 181 SRAELKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIATIHGEGYRFCGDLE 237
+RA+LLKKMTGRELKPHDRTVDVTIRRIRKHFES TPEI+ATIHGEGYRFCGDLE
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRIRKHFESVSGTPEIATIHGEGYRFCGDLE 237

>yvu:VV10548 fexA; aerobic respiration control protein FexA [KO:K02483]
Length = 238

Score = 411 bits (1056), Expect = e-114
Identities = 205/237 (86%), Positives = 218/237 (91%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLVIMD1NLPGK 60
MQTP ILIVEDE VTRNTLKS1FEAEGY VFEA++G EMH +LSE INLVIMD1NLPGK
Sbjct: 1 MQTPQILIVEDEQVTRNTLKS1FEAEGYAVFEASNGDEMHHMLSENS1NLVIMD1NLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
+M+ + EE+RSVE Y+FNGW LD1NSRSL1 P G+ YKLPSEFRA+LHFCENPGK1Q
Sbjct: 121 SMSSSVMPPEEKRSVEKYEFGNGWVL1NSRSL1SPSGDGYKLPSEFRALLHFCENPGK1Q 180

Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11ATIHGEGYRFCGDLE 237
+RA+LLKKMTGRELKPHDRTVDVT1RR1RKHFES TPE11ATIHGEGYRFCGDLE
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVT1RR1RKHFESVSGTPE11ATIHGEGYRFCGDLE 237

>pmu:PM0219 arcA; aerobic respiration control protein [KO:K02483]
Length = 236

Score = 394 bits (1011), Expect = e-108
Identities = 194/237 (81%), Positives = 210/237 (88%), Gaps = 1/237 (0%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLVIMD1NLPGK 60
M TP ILIVEDE +TRNTLKS1FEAEGY+VFEA DGA+MH+ILS INLVIMD1NLPGK
Sbjct: 1 MGTPQILIVEDEA1TRNTLKS1FEAEGYEVFEADGAQMHRILSNK1NLVIMD1NLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLSR 120
NGL+LARELRE N ALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLL R
Sbjct: 61 NGMLMLARELRETTNTALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLQR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
TM + + +E Y+FNGW LD+NSR+LI P+GE+YKLPSEFRAMLHFCENPGK1Q
Sbjct: 121 TMQENS-KDSHHPIEQYRFNGWTLDNSRTL1NPEGEEYKLPSEFRAMLHFCENPGK1Q 179

Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11ATIHGEGYRFCGDLE 237
+R ELLKKMTGRELK P DRTVDVT1RR1RKHFES P+TPE11ATIHGEGYRFCG+LE
Sbjct: 180 TREELLLKKMTGRELK P QDRTVDVT1RR1RKHFEDHPETPE11ATIHGEGYRFCGELE 236

>son:S03988 arcA; aerobic respiration control protein ArcA [KO:K02483]
Length = 238

Score = 392 bits (1006), Expect = e-108
Identities = 194/238 (81%), Positives = 209/238 (87%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYD1NLVIMD1NLPGK 60
MQ PHILIVEDE VTRNTL+S1FEAEGY V EA DGAEMH+ + E INLV+MD1NLPGK
Sbjct: 1 MQNPHILIVEDEAVTRNTLRS1FEAEGYVVTAEANDGAEMHKAMQENK1NLVIMD1NLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLSR 120
NGLLLARELRE N+ L+FLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLL+R
Sbjct: 61 NGLLLARELREINNIGL1FLTGRDNEVDKILGLE1GADDY1TKPFNPRELTIRARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPSEFRAMLHFCENPGK1Q 180
+ G EE+ SVE Y+FN W L+1NSRSL+ P GE YKLPSEFRAMLHF ENPGK1
Sbjct: 121 VNSAGNEVEEKSSVEYYRFNDWSLE1NSRSLVSPQGESYKLPSEFRAMLHFV1ENPGK1L 180

Query: 181 SRAELKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11ATIHGEGYRFCGDLED 238
+RA+LL KMTGRELKPHDRTVDVT1RR1RKHFES PDTPE11ATIHGEGYRFCG+LED
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVT1RR1RKHFESLPDTPE11ATIHGEGYRFCGNLED 238

>msu:MS1504 ompR; response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain [KO:K02483].
Length = 236

Score = 382 bits (982), Expect = e-105
Identities = 190/240 (79%), Positives = 209/240 (87%), Gaps = 7/240 (2%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYDINLVIMDINLPGK 60
M +P ILIVEDE VTRNTLKS1FEAEGY+VFEATDG +MHQ1+ +INLV+MDINLPGK
Sbjct: 1 MLSPQ1LIVEDETTRNTLKS1FEAEGYEVFEATDGNQMHQ11ETQE1NLVVMIDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120
NGL+LARELRE+ N ALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPREL 1RARNLL R
Sbjct: 61 NGMLLARELREKNTALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELA1RARNLLHR 120

Query: 121 TMNLGTVSEERRS—VESYKFNGWELD1NSRSL1GPDGEQYKLPRSEFRAMLHFCENPG 177
TM E+ S V++Y+FNGW LD1N R+L1 P+ +YKLPRSEFRAMLHFCENPG
Sbjct: 121 TM—AENEKNSNTHVDAYRFNGWTL1DKRAL1DPESVEYKLPRSEFRAMLHFCENPG 176

Query: 178 KIQSRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11ATIHGEGRFCGDLE 237
KIQ+R +LLKKMTGRELKP DRTVDVT1RR1RKHF E PDTPE11ATIHGEGRFCG++E
Sbjct: 177 KIQTREDLLKKMTGRELKPHDRTVDVT1RR1RKHFEDHPDTPE11ATIHGEGRFCGE1E 236

>hdu:HDO278 arcA; aerobic respiration control protein ArcA [KO:K02483]
Length = 237

Score = 377 bits (968), Expect = e-103
Identities = 188/237 (79%), Positives = 204/237 (86%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYDINLVIMDINLPGK 60
MQ P ILIVEDELVTRNTLKS1FEAEGY+VFEA+DG EM+ IL++ INLVIMDINLPGK
Sbjct: 1 MQNPQ1LIVEDELVTRNTLKS1FEAEGYEVFEASDGT1LAQQT1NLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120
NGL+LARELRE +ALMFLTGRDNEVDK1LGLE+GADDY1TKPFNPRELT1RARNLL R
Sbjct: 61 NGMLLARELRENTKMLMFLTGRDNEVDK1LGLEVGADDY1TKPFNPRELT1RARNLLHR 120

Query: 121 TMNLGTVSEERRSVESYKFNGWELD1NSRSL1GPDGEQYKLPRSEFRAMLHFCENPGK1Q 180
TM ESY+FNGW LD+NSRSL1 P+GE KLPRSEFRA+LHFCENPGK1Q
Sbjct: 121 TMLEKDKVSHSEQQESYRFNGWTL1DVNSRSL1TPEGE1NKLPSEFRALLHFCENPGK1Q 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVT1RR1RKHFESTPDTPE11ATIHGEGRFCGDLE 237
+R +LL KMTGRELKPHDRTVDVT1RR1RKHF E +TPE11 TIHGEGRFCG +E
Sbjct: 181 TREDLLKKMTGRELKPHDRTVDVT1RR1RKHFEDHLNTPE11VTIHGEGRFCGQ1E 237

>hin:H10884 arcA; aerobic respiration control protein arcA homolog [KO:K02483]
Length = 236

Score = 374 bits (960), Expect = e-103
Identities = 183/237 (77%), Positives = 206/237 (86%), Gaps = 1/237 (0%)

Query: 1 MQTPHILIVEDELVTRNTLKS1FEAEGYDVFEATDGAEMHQ1LSEYDINLVIMDINLPGK 60
M TP IL+VEDE+VTRNTLK 1FEAEGYDVFEA +G EMH IL+ ++INLV+MDINLPGK
Sbjct: 1 MTTPK1LVEDE1VTRNTLKG1FEAEGYDVFEAENGVEMHH1LANHN1NLVVMIDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDK1LGLE1GADDY1TKPFNPRELT1RARNLLSR 120
NGLLLARELRE+ ++ L+FLTGRDNEVDK1LGLE1GADDY+TKPFNPRELT1RARNLL R

Sbjct: 61 NGLLLARELREELSLPLIFLTGRDNEVDKILGLEIGADDYLTKPFNPRLTIRARNLLHR 120
Query: 121 TMNLGTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPRLPRSEFRAMLHFCENPGKIQ 180
M E E Y+FNGW+LD+NS SLI P+G+++KLPRLPRSEFRAMLHFCENPGK+Q
Sbjct: 121 AMP-HQEKEKNTFGREFYRFNGWKLQLDLSHSLITPEGQEFLKLPRLPRSEFRAMLHFCENPGKIQ 179
Query: 181 SRAELKKMTGRELKPHDRDVTIRRIKHFESTPDTEIIATIHGEGYRFGDLE 237
+R ELLKKMTGRELKPHDRDVTIRRIKHFESTPDTEIIATIHGEGYRFGDLE
Sbjct: 180 TREELKKMTGRELKPKDRTVDVTIRRIKHFEDHPNTPNIIMTIHGEGYRFGDIE 236

>vfi:VF1570 torR; TorCAD operon transcriptional regulatory protein TorR
[KO:KO2483]
Length = 232

Score = 217 bits (552), Expect = 2e-55
Identities = 110/231 (47%), Positives = 152/231 (65%), Gaps = 2/231 (0%)

Query: 5 HILIVEDELVTRNTLKSIFEAEQYDVFEATDGAEMHQILSEYDINLVIMDINLPGKNGLL 64
HIL+VEDE+VTR+ L FEAEGY V EA GAEM IL+E ++L+++DINLPG++GLL
Sbjct: 4 HILVVEDEVVTRSKLVGYFEAEQYQVSEAETGAEMRSILAEQKVDLIMLDINLPGEDGLL 63
Query: 65 LARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRLTIRARNLLSRTMNL 124
LARELR Q+N+ ++ +TGR + +D+I+GLE+GADDY+TKP REL +R +NL R M+L
Sbjct: 64 LARELRSQSNIGIILVTGRTDSIDRIVGLEMGADDYVTKPVELRELLVRVKNLFWR-MSL 122
Query: 125 GTVSEERRSVESYKFNGWELDINSRSLIGPDGEQYKLPRLPRSEFRAMLHFCENPGKIQSRAE 184
E +F W DI R+L +GE KL ++E+ ++ P + SR
Sbjct: 123 ANEPVELDESNVVRGEWTFD1QRRAL-SNNGEPVKLTKAELYLLVALSSYPNTVLSRER 181
Query: 185 LLKKMTGRELKPHDRDVTIRRIKHFESTPDTEIIATIHGEGYRFGD 235
+L ++ R P+DRT+DV IRR+R E P P+I T+HGEGY F GD
Sbjct: 182 ILNMISHRVDAPNDRTIDVLIRRMRAKMEVDPKNPQIFVTVHGEGYMFAGD 232

Database: GENES+DGENES: GENES+DGENES(amino acid sequence)
Posted date: Jun 6, 2005 5:28 AM
Number of letters in database: 319,922,540
Number of sequences in database: 911,393

Database: dgenes
Posted date: Jun 4, 2005 8:12 AM
Number of letters in database: 217,783,082
Number of sequences in database: 493,871

Lambda K H
0.319 0.138 0.396

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 249,767,882
Number of Sequences: 1405264
Number of extensions: 9983109
Number of successful extensions: 34529
Number of sequences better than 10.0: 30
Number of HSP's better than 10.0 without gapping: 3346
Number of HSP's successfully gapped in prelim test: 1949
Number of HSP's that attempted gapping in prelim test: 26334

Number of HSP's gapped (non-prelim): 5566
length of query: 238
length of database: 537,705,622
effective HSP length: 121
effective length of query: 117
effective length of database: 367,668,678
effective search space: 43017235326
effective search space used: 43017235326
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 72 (32.3 bits)